

XX WP1: 2002-025882/03.
 DR CXC receptor 4 agonists that reduces hematopoietic cell multiplication
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or
 PT peripheral blood stem cell transplantation
 XX
 PS Claim 8; Page 58; 74pp: English.
 XX
 CC The sequences given in AAB47680-717 represent peptides which may be
 CC used in the method of the invention for reducing the rate of
 CC hematopoietic cell multiplication. These peptides act as CXC chemokine
 CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
 CC stromal cell derived factor one (SDF-1) with some also containing
 CC sequences derived from macrophage inflammatory protein 1-alpha
 CC (MIP-1-alpha). They can be used to reduce susceptibility of the
 CC hematopoietic cells to a cytotoxic agent, by administering one of the
 CC agonist peptides to the cells prior to or during exposure of the
 CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
 CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly
 CC in a patient with cancer requiring autologous or allogeneic bone marrow
 CC or peripheral blood stem cell transplantation, or an autoimmune disease.
 XX
 SQ Sequence 31 AA:
 Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVSLSYRCPCRFPGGGGLKWIQYLERKALN 31
 DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLERKALN 31
 RESULT 2
 ID AAB47693 standard; peptide; 31 AA.
 XX AAB47693;
 AC 30-JAN-2002 (first entry)
 DT SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.
 DE
 XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX WO200176615-A2.
 PN 18-OCT-2001.
 PD 12-APR-2001; 2001WO-CA00540.
 XX 12-APR-2001; 2000CA-2305036.
 PF 14-SEP-2000; 2000US-232425P.
 PR 23-FEB-2001; 2001CA-2335109.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
 PI Cashman J, Clark-Lewis I;
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PS Example 1; Page 42; 74pp: English.
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 XX
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 Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVSLSYRCPCRFPGGGGLKWIQYLERKALN 31
 DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLERKALN 31
 RESULT 3
 ID AAB47695 standard; peptide; 31 AA.
 XX AAB47695;
 AC 30-JAN-2002 (first entry)
 DT SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.
 DE
 XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 XX WO200176615-A2.
 PN 18-OCT-2001.
 PD 12-APR-2001; 2001WO-CA00540.
 XX 12-APR-2001; 2000CA-2305036.
 PF 14-SEP-2000; 2000US-232425P.
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Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31

RESULT 4
AAB47700 standard; peptide; 31 AA.

AC AAB47700;
DT 30-JAN-2002 (first entry)
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic acid.
KM Hematopoietic cell; multiplication; CXc chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 24..28
FT /note= "Joined by side chain cyclization using lactam formation"
PN MO200176615-A2.
PD 18-OCT-2001.
PE 12-APR-2001; 2001WO-CA00540.
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
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Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPGRFFGGGLKWIQYLEKALN 31

RESULT 5
AAB47701 standard; peptide; 31 AA.

AC AAB47701;
DT 30-JAN-2002 (first entry)
DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic acid.
KM Haematopoietic cell; multiplication; CXc chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 20..24
FT /note= "Joined by side chain cyclization using lactam formation"
PN MO200176615-A2.
PD 18-OCT-2001.
PE 12-APR-2001; 2001WO-CA00540.
PR 12-APR-2000; 2000CA-2305036.
PR 14-SEP-2000; 2000US-232425P.
PR 23-FEB-2001; 2001CA-2335109.
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CC (MIP-1-alpha). They can be used to reduce susceptibility of
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Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPRCFFGGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPRCFFGGGGLKWIQYLEKALN 31

RESULT 6

AAB47702
ID AAB47702 standard; peptide; 31 AA.

AC AAB47702;

DI 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

XX Haematopoietic cell; multiplication; CXCR4; CXCR4;
XX agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
XX macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
XX autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 24..28 /note= "Joined by side chain cyclization using
FT lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

FT MO200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001MO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

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PI Cashman J, Clark-Lewis I;

PI WPI; 2002-025882/03.

XX Example 1; Page 43; 74pp; English.

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CC stromal cell derived factor one (SDF-1) with some also containing

CC sequences derived from macrophage inflammatory protein 1-alpha
CC (MIP-1-alpha). They can be used to reduce susceptibility of
CC hematopoietic cells to a cytotoxic agent, by administering one of the
CC agonist peptides to the cells prior to or during exposure of the
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
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SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPRCFFGGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPRCFFGGGGLKWIQYLEKALN 31

RESULT 7

AAB47703
ID AAB47703 standard; peptide; 31 AA.

AC AAB47703;

DI 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

XX Haematopoietic cell; multiplication; CXCR4; CXCR4;
XX agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
XX macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
XX autologous; allogenic; bone marrow; stem cell; transplantation.
XX
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 20..24 /note= "Joined by side chain cyclization using
FT lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

FT MO200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001MO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

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PI WPI; 2002-025882/03.

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CC hematopoietic cell multiplication. These peptides act as CXCR4
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
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CC sequences derived from macrophage inflammatory protein 1-alpha
 CC (MIP-1-alpha). They can be used to reduce susceptibility of
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 Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
 DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
 RESULT 8
 AAB47706
 ID AAB47706 standard; peptide; 31 AA.
 AC AAB47706;
 DX 30-JAN-2002 (first entry)
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-C9/C11-cyclic acid.
 XX
 KM Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KM autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Disulfide-bond 9..11
 PN WO200176615-A2.
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-CA00540.
 XX
 PR 12-APR-2000; 2000CA-2305036.
 PR 14-SEP-2000; 2000US-232425P.
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 PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
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 DR WPI; 2002-025882/03.
 XX
 PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication
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 PS
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 CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on
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 SQ Sequence 31 AA:
 Query Match 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
 DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
 RESULT 9
 AAB47707
 ID AAB47707 standard; peptide; 31 AA.
 AC AAB47707;
 DX 30-JAN-2002 (first entry)
 DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-C9/C11-cyclic amide.
 XX
 KM Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;
 KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KM autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Disulfide-bond 9..11
 FT Modified-site 31
 FT /note="C-terminal amide"
 PN WO200176615-A2.
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-CA00540.
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 Best Local Similarity 100.0%; Pred. No. 1.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPRCFRFGGGLKWIQETLEKALN 31
 1 KPVSLSYRCPRCFRFGGGLKWIQETLEKALN 31
 DB

RESULT 10
 AAB47714
 ID AAB47714 standard; peptide: 31 AA.

AC AAB47714;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.

XX Haematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;
 KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.

PN W0200176615-A2.

PD 18-OCT-2001.

PE 12-APR-2001; 2001WO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KPVSLSYRCPRCFRFGGGLKWIQETLEKALN 31
 1 KPVSLSYRCPRCFRFGGGLKWIQETLEKALN 31
 DB 1 KPVSLSYRCPRCFRFGGGLKWIQETLEKALN 31

RESULT 11
 AAB47715
 ID AAB47715 standard; peptide: 31 AA.

AC AAB47715;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.

XX Haematopoietic cell; multiplication; CXK chemokine receptor 4; CXCR4;
 KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
 KW autologous; allogenic; bone marrow; stem cell; transplantation.
 XX
 OS Synthetic.

FN Key Location/Qualifiers
 FT Modified-site 31
 /note="C-terminal amide"

PN W0200176615-A2.

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 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPRCFRFGGGLKWIQETLEKALN 31

Db 1 KPVSLSYRCPCRFPGGGGLKWIQEIYLEKALN 31

RESULT 12

ABAB7716 ID ABA47716 standard; peptide: 31 AA.

AC ABA47716;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

KW Haematopoietic cell; multiplication; CXCR chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 24..28 /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

PN WO200176615-A2.

PD 18-OCT-2001.

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PR 12-APR-2000; 2000CA-2305036.

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XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

XX Example 1; Page 47; 74pp; English.

XX The sequences given in ABA47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXCR chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFPGGGGLKWIQEIYLEKALN 31

Db 1 KPVSLSYRCPCRFPGGGGLKWIQEIYLEKALN 31

RESULT 13

ABAB7717 ID ABA47717 standard; peptide: 31 AA.

AC ABA47717;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

KW Haematopoietic cell; multiplication; CXCR chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 20..24 /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

PN WO200176615-A2.

PD 18-OCT-2001.

PE 12-APR-2001; 2001WO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

PI Cashman J, Clark-Lewis I;

DR WPI: 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

XX Example 1; Page 47; 74pp; English.

XX The sequences given in ABA47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXCR chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFPGGGGLKWIQEIYLEKALN 31

Db 1 KPVSLSYRCPCRFPGGGLKWIQDYLERALN 31

RESULT 14

AA047704 standard; peptide: 31 AA.

AA047704;

30-JAN-2002 (first entry)

SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic acid.

Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation. Synthetic.

Key Location/Qualifiers

Modified-site 20..24 /note= "Joined by side chain cyclization using lactam formation"

Misc-difference 24 /label= E24D

Modified-site 24..28 /note= "Can be joined by side chain cyclization using lactam formation"

WO200176615-A2.

18-OCT-2001.

12-APR-2001; 2001WO-CA00540.

12-APR-2000; 2000CA-2305036.

14-SEP-2000; 2000US-232425P.

23-FEB-2001; 2001CA-2335109.

(UYBR-) UNIV BRITISH COLUMBIA.

(CHEM-) CHEMOKINE THERAPEUTICS CORP.

Safari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

Cashman J, Clark-Lewis I;

WPI; 2002-025882/03.

Example 1; Page 44; 74pp; English.

The sequences given in AA047680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the cells to the cytotoxic agent, prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

Sequence 31 AA;

Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5.1e-17;

Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KPVSLSYRCPCRFPGGGLKWIQDYLERALN 31

Db 1 KPVSLSYRCPCRFPGGGLKWIQDYLERALN 31

RESULT 15

AA047705 standard; peptide: 31 AA.

AA047705;

30-JAN-2002 (first entry)

SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic amide.

Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation. Synthetic.

Key Location/Qualifiers

Modified-site 20..24 /note= "Joined by side chain cyclization using lactam formation"

Misc-difference 24 /label= E24D

Modified-site 24..28 /note= "Can be joined by side chain cyclization using lactam formation"

Modified-site 31 /note= "C-terminal amide"

WO200176615-A2.

18-OCT-2001.

12-APR-2001; 2001WO-CA00540.

12-APR-2000; 2000CA-2305036.

14-SEP-2000; 2000US-232425P.

23-FEB-2001; 2001CA-2335109.

(UYBR-) UNIV BRITISH COLUMBIA.

(CHEM-) CHEMOKINE THERAPEUTICS CORP.

Safari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

Cashman J, Clark-Lewis I;

WPI; 2002-025882/03.

Example 1; Page 44; 74pp; English.

The sequences given in AA047680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the cells to the cytotoxic agent, prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

Db 1 KPVSLSYRCPCRFPGGGLKWIQDYLERALN 31

RESULT 14
AAB47704

AB47704 standard; peptide: 31 AA.

AC AAB47704;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic acid.

KW Haematopoietic cell; multiplication; CXc chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease;

KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;

KW autologous; allogenic; bone marrow; stem cell; transplantation.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 20..24

FT /note= "Joined by side chain cyclization using lactam formation"

FT Misc-difference 24 /label= E24D

FT Modified-site 24..28

FT /note= "Can be joined by side chain cyclization using lactam formation"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSLSYRCPCRFPGGGLKWIQDYLERALN 31

Db 1 KPVSLSYRCPCRFPGGGLKWIQDYLERALN 31

RESULT 15
AAB47705

AB47705 standard; peptide: 31 AA.

AC AAB47705;

DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/D24-cyclic amide.

KW Haematopoietic cell; multiplication; CXc chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease;

KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;

KW autologous; allogenic; bone marrow; stem cell; transplantation.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 20..24

FT /note= "Joined by side chain cyclization using lactam formation"

FT Misc-difference 24 /label= E24D

FT Modified-site 24..28

FT /note= "Can be joined by side chain cyclization using lactam formation"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

FT /note= "C-terminal amide"

FT Modified-site 31

Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5,1e-17;

Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5,1e-17;

XX	Sequence	31 AA;
SQ		

Query Match	98.3%	Score 172;	DB 23;	Length 31;
Best Local Similarity	96.8%;	Pred. No. 5.1e-17;		
Matches 30;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 KPVSLSYRCPRRFFGGGGLKWIQDYLEKALN 31
        | | | | | | | | | | | | | | | |
DB      1 KPVSLSYRCPRRFFGGGGLKWIQDYLEKALN 31

```

Search completed: October 9, 2003, 09:19:01
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:42; Search time 39 Seconds

(without alignments)
76.442 Million cell updates/sec

Title: US-09-835-107A-11

Perfect score: 175

Sequence: 1 KPVSLSYRCPGCRFFGGGLMKIQLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	66.9	89	2	A53497
2	117	66.9	89	2	I53416
3	117	66.9	93	2	G01540
4	117	66.9	93	2	T81182
5	61	34.9	1088	2	T08583
6	61	34.9	1088	2	H84604
7	60.5	34.6	974	2	T10797
8	58	33.1	469	2	C83345
9	58	33.1	1081	2	T52028
10	56	32.0	233	2	T55594
11	54	30.9	398	2	T52311
12	53	30.3	454	2	C64104
13	53	30.3	470	2	T46814
14	53	30.3	470	2	B95419
15	50	28.6	202	2	A13489
16	50	28.6	588	2	S34786
17	50	28.6	685	2	T10800
18	49.5	28.3	170	2	B85359
19	49.5	28.3	577	2	T50731
20	49	28.0	386	2	C81415
21	49	28.0	508	2	F81198
22	49	28.0	517	2	A70793
23	49	28.0	556	1	A53376
24	49	28.0	557	1	A25493
25	49	28.0	1722	2	A88470
26	48	27.4	189	2	D68389
27	48	27.4	309	1	S34198
28	48	27.4	331	1	LNM58R
29	48	27.4	383	2	C90136

30	48	27.4	593	2	S30958
31	48	27.4	661	2	S45131
32	48	27.4	1016	2	F82159
33	48	27.4	1429	2	S06434
34	47.5	27.1	439	2	E72298
35	47.5	27.1	722	2	H95986
36	47	26.9	203	2	I50481
37	47	26.9	388	2	S30901
38	47	26.9	409	2	S01825
39	47	26.9	623	2	T40685
40	47	26.9	1108	2	T35827
41	47	26.9	1400	2	T22544
42	46.5	26.6	1112	2	D96753
43	46.5	26.6	1287	2	T22235
44	46	26.3	122	2	T45165
45	46	26.3	212	2	S73466

ALIGNMENTS

RESULT 1

pre-B-cell growth-stimulating factor precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence-revision 02-Jun-1994 #text-change 20-Jun-2000

C:Accession: A53497, I59582

R:Nagasawa, T.; Kikuchi, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994

A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.

A:Reference number: A53497; MUID:94181581; PMID:8134392

A:Accession: A53497.

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-89 <NAC>

A:Cross-references: GB:D21072; NID:9413905; PIDN:BA04648.1; PID:9468457

R:Tashiro, K.; Tada, H.; Hellker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993

A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me

A:Reference number: I59582; MUID:3342488; PMID:8342023

A:Accession: I59582

A:Status: preliminary; translated from GB/EMBL/DBEST

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: GB:L12029; NID:9393179; PIDN:AAA40100.1; PID:9393180

C:Genetics:

A:Gene: SDF-1-alpha

A:Superfamily: beta-thromboglobulin

C:Keywords: cytokine

Query Match 66.9%; Score 117; DB 2; Length 89;

Best local similarity 40.3%; Pred. No. 4.8e-09;

Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

Qy 1 KPVSLSYRCPGCRFFGG-----GLKIQE 24

Db 22 KPVSLSYRCPGCRFFGSHIARANKHLKILTPNCALQIVARLKNRNRQVCDIKKWKID 81

Qy 25 YLEKALN 31

Db 82 YLEKALN 88

RESULT 2

I53416

Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)

C>Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 05-Nov-1999

C:Accession: I53416

R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994

A:Title: Molecular cloning of TP861, a gene whose expression is repressed by the tumor

A:Reference number: I53416; MUID:95073497; PMID:7962471

A:Accession: I53416 translated from GB/EMBL/DBJ
A:Status: Preliminary;
A:Molecule type: mRNA
A:Residues: 189 <RSS>
C:Cross-references: GB:S74318; NID:g786393; PIDN:AA32650.1; PID:g786394
C:Genetics
A:Gene: TPARI
A:Superfamily: beta-thromboglobulin

QY	1	KPVSLSYRCDCRFFFGG-----GGLEKWIQ	24
Db	22	KPVSLSYRCDCRFFESHIPANVYKHILKILNTPCALQIVARLEKNNNNROYCIDPKLEKWIQ	81
QY	25	YLEKALN 31	
Db	82	YLEKALN 88	

```
QY 1 KPVLSYRQPCRFEGG-----GGLMKIOE 24
    |||||
Db 22 KPVLSYRQPCRFEGSHVARYNKHILKILMTPNCALQIVARLKNRNRQVODIPKXWID 81
    |||||
QY 25 YLEKALN 31
    |||||
Db 82 YLEKALN 88
```

QY	1	KPVSLSTRCPREFGG-----	OGKMWIOE 2
Db	22	KPVSLSTRCPREFESHIANRYNKHILMTPNCALQIVARLKNNNPROVCIDRKLXWIOE	81
QY	25	YLERALN 31	
Db	82	YLERALN 88	

```
QY      3 VLSYRCPCRFFGGGLKMIQY 25
      : || || : ||||| : :
Db     833 IFLSRHCPIMWGYGGGLKMLERF 855
```

Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VLSYRCPCRFPGGGLKMWIOEY 25
: || || : ||||| :
Db 837 IFLSRHCPIMWYGGLKMWLEF 859

RESULT 7

T10797

cellulose synthase (EC 2.4.1.-) catalytic chain celA1 - upland cotton

C:Species: Gossypium hirsutum (upland cotton)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10797

R:Pear, J.R.; Kawagoe, Y.; Schreckengost, W.E.; Delner, D.P.; Stalker, D.M.

Proc. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996

A:Title: Higher plants contain homologs of the bacterial celA genes encoding the catalytic

A:Reference number: 217152; MUID:97057296; PMID:8901635

A:Accession: T10797

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-974 <PEA>

A:Cross-references: EMBL:U58283; NID:q1706955; PIDN:AA837766.1; PID:q1706956

A:Experimental source: strain Acala SJ-2; fiber

C:Genetics:

A:Gene: celA1

C:Function: involved in the synthesis of cellulose

A:Keywords: glycosyltransferase; hexosyltransferase

Query Match

Best Local Similarity 34.6%; Score 60.5; DB 2; Length 974;

Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VLSYRCPCRF-FGGGGLKMWIQ 23

Db 721 IFLSRHCPIMWYGGLKMWIQ 742

RESULT 8

C83345

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83345

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim,

.; Lory, S.; Olson, M.Y.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437357; PMID:10984043

A:Accession: C83345

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-469 <STO>

A:Cross-references: GB:AE004668; GB:AE004091; NID:g9948446; PIDN:AA05801.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2413

Query Match

Best Local Similarity 33.1%; Score 58; DB 2; Length 469;

Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFPGGGLKMWIOEYLEKALN 31

Db 199 PYPDYRCPCFGLGEGAGVAKNLHYLENLNLN 228

RESULT 9

T52028

cellulose synthase [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T52028

R:Josh, C.

submitted to the EMBL Data Library, May 1998

A:Reference number: 225890

A:Accession: T52028

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1081 <JOS>

A:Cross-references: EMBL:AF062485; PIDN:AA029067.1

Query Match

Best Local Similarity 33.1%; Score 58; DB 2; Length 1081;

Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLSYRCPCRFPGGGLKMWIO 23

Db 831 IFLSRHCPIMWYGGLKMWLE 851

RESULT 10

T35594

hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000

C:Accession: T35594

R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: 221583

A:Accession: T35594

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <SAU>

A:Cross-references: EMBL:AL031117; PIDN:CAA20421.1; GSPDB:GN00070; SC6DB:SC6G4.43c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SC6DB:SC6G4.43c

C:Superfamily: hypothetical protein HI0278

Query Match

Best Local Similarity 32.0%; Score 56; DB 2; Length 233;

Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 6 SYRCPCRFPGG-GGLKMWIOEYLEK 28

Db 135 SGRIPCRFTFGHMGEPKVRKRMEX 159

RESULT 11

T52311

isopenicillin N epimerase [validated] - Streptomyces clavuligerus

C:Species: Streptomyces clavuligerus

C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T52311

R:Kovacevic, S.; Tobin, M.B.; Miller, J.R.

J. Bacteriol. 172, 3952-3958, 1990

A:Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deaceto

A:Reference number: 226033; MUID:90299822; PMID:1694525

A:Accession: T52311

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-398 <KOV>

A:Cross-references: EMBL:M32324; PIDN:AA26714.1

C:Genetics:

A:Gene: cetD

Query Match

Best Local Similarity 30.9%; Score 54; DB 2; Length 398;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 RCPCRFPGGGLKMWI 22

Db 205 RIPCDFYAGSGHKL 219

RESULT 12

C64104
gamma-aminobutyrate aminotransferase (EC 2.6.1.-) - Haemophilus influenzae (strain Rd KM
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: C64104; J05879
R:Reischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirness, E.F.; Kerlavage, R.
J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fabe, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
Science 269, 436-512, 1995
A:Authors: Guelth, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64104
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-454 <TIGR>
A:Cross-References: GB:U02776; GB:U42023; NID:91573969; PIDN:AA022610.1; PID:91573974; T
R:Ikai, H.; Yamamoto, S.
Biol. Pharm. Bull. 21, 170-173, 1998
A:Title: Two genes involved in the 1,3-diaminopropane production pathway in Haemophilus
A:Reference number: J05879; MUID:98173550; PMID:9514614
A:Accession: J05879
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-454 <IKA>
A:Cross-References: GB:U02776; NID:91573969; PIDN:AA022610.1; PID:91573974
C:Comment: This enzyme is involved in the pathway of 1,3-diaminopropane synthesis.
C:Genetics:
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
C:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
F:287/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match

Best Local Similarity 30.3%; Score 53; DB 2; Length 454;
Best Local Similarity 38.5%; Pred. NO. 15;
Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 PVSLSYRCPGRFGGGGKLTIOETLE 27
DB 181 PYPHYRCPGRFGGGGAKKAYEQYFE 206

RESULT 13

T46814
gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhaA [imported] - Rhizobium meliloti
C:Species: Rhizobium meliloti
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
C:Accession: T46814
R:Lynech, D.; O'Connell, M.; O'Brien, J.
submitted to the EMBL Data Library, December 1998
A:Description: Cloning and sequence analysis of the Sinorhizobium meliloti 2011 rhaA gene
A:Reference number: Z24097
A:Accession: T46814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-470 <LNU>
A:Cross-References: EMBL:AF110737; PIDN:AA094412.1
A:Experimental source: strain 2011
C:Genetics:
A:Gene: rhaA
C:Function:
A:Pathway: siderophore biosynthesis
C:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase

Query Match

Best Local Similarity 30.3%; Score 53; DB 2; Length 470;
Best Local Similarity 43.8%; Pred. NO. 16;
Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPGRFGGGG---LKWIOETLEKAL 30
DB 181 PYPHYRCPGRFGGGG---LKWIOETLEKAL 30

DB 198 PYPHYRCP---FGRGNETATLAETFEFAL 226

RESULT 14

B95419
diaminobutyrate-pyruvate transaminase (EC 2.6.1.46) RhaA [imported] - Sinorhizobium m
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 02-Aug-2002
C:Accession: B95419
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Kemp, C.; Abola, A.P.; Barlow-Hubler, F.; B
J.; Kalmn, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: B95419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <KUR>
A:Cross-References: GB:AB006469; PIDN:AA065916.1; PID:914524429; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hub
pela, D.; Chailu, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalmn, S.; Keating, D.H.; Kiss, E.; Kemp, C.; Leila
hebaull, P.; Vandenbol, M.; Votholier, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A60359; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: rhaA
A:Superfamily: beta-alanine-pyruvate transaminase
C:Keywords: aminotransferase

Query Match

Best Local Similarity 30.3%; Score 53; DB 2; Length 470;
Best Local Similarity 43.8%; Pred. NO. 16;
Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPGRFGGGG---LKWIOETLEKAL 30
DB 198 PYPHYRCP---FGRGNETATLAETFEFAL 226

RESULT 15

A13489
cytochrome c-552 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 02-Apr-2002
C:Accession: A13489
R:Delvecchio, V.G.; Kapprahl, V.; Redgar, R.J.; Patra, G.; Muler, C.; Los, T.; Ivanov
.; Marut, M.; Goldman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: A03252; PMID:11756688
A:Accession: A13489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-References: GB:AF008917; PIDN:AAU53084.1; PID:917983947; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11903
A:Map position: 1
C:Superfamily: membrane-bound cytochrome c/cytochrome c homolog
C:Keywords: chromoprotein; heme; iron; metalloprotein
F:84/87/Binding site: heme (His) (axial ligand) #status predicted
F:88/Binding site: heme iron (His) (axial ligand) #status predicted
F:153/Binding site: heme iron (Met) (axial ligand) #status predicted

Query Match

Best Local Similarity 28.6%; Score 50; DB 2; Length 202;
Best Local Similarity 44.0%; Pred. NO. 19;
Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Thu Oct 9 16:39:00 2003

us-09-835-107a-11.rpr

Page 5

Oy 6 SYRCPRRFFGGGGLKWIQEIYERKAL 30
|| : || | | : | |
Db 117 SYSAAMKEFGAGAGNKNKWDPEHINKEL 141

Search completed: October 9, 2003, 09:21:32
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 9, 2003, 09:17:41 ; Search time 22 Seconds
(without alignments)
66.265 Million cell updates/sec

Title: US-09-835-107A-11

Perfect score: 175
Sequence: 1 KPVSLSYRCPQFFGGGGLKWIQYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	1	SDPL_MOUSE
2	117	66.9	93	1	SDPL_FELCA
3	117	66.9	93	1	SDPL_HUMAN
4	54	30.9	397	1	CEPD_STREL
5	54	30.9	955	1	B3A4_RABIT
6	53	30.3	454	1	DAT_HABIN
7	53	30.3	470	1	REBA_RHIME
8	53	30.3	529	1	PDP2_HUMAN
9	52	29.7	983	1	B3A4_HUMAN
10	51	29.1	282	1	HGCC_HUMAN
11	50	28.6	530	1	PDP2_RAT
12	49	28.0	508	1	GLPK_MYCLE
13	49	28.0	517	1	GLPK_MYCTU
14	49	28.0	557	1	TR2M_PESS
15	49	28.0	1714	1	YP93_CAEEL
16	48.5	27.7	257	1	PEBB_PROMA
17	48	27.4	331	1	PEBB_MOUSE
18	48	27.4	593	1	VG13_BPMLS
19	48	27.4	661	1	PDAT_YEAST
20	48	27.4	1429	1	LI12_CAEEL
21	47.5	27.1	430	1	TCO2_MOUSE
22	47	26.9	203	1	SN2B_CARAU
23	47	26.9	388	1	CEPD_NOCILA
24	47	26.9	409	1	TGF3_PIG
25	47	26.9	507	1	GLK2_STRCO
26	47	26.9	623	1	PDAT_SCHPO
27	46	26.3	212	1	Y010_MYCPN
28	46	26.3	390	1	ACKA_MYCPN
29	45.5	25.7	387	1	KR16_HSV1
30	45	25.7	351	1	KAP1_APLCA
31	45	25.7	373	1	DNAU_CAMJE
32	45	25.7	359	1	ACKA_MTCGE
33	45	25.7	577	1	Y04B_CAEEL

34	45	25.7	577	1	SVL_AOUPI	O9xmd3 aquifex pyr
35	45	25.7	1142	1	JAK1_HUMAN	P23458 homo sapien
36	45	25.7	1153	1	JAK1_MOUSE	P52332 mus musculus
37	44.5	25.4	198	1	MYR_MITCE	P39047 mltrocoma c
38	44.5	25.4	288	1	EPG_RALSO	Q892d7 raltosoma s
39	44.5	25.4	501	1	TRA2_HUMAN	Q12933 homo sapien
40	44.5	25.4	511	1	FAST_MOUSE	O9jix9 mus musculus
41	44	25.1	322	1	V493_AOUAE	O66783 aquifex aeo
42	44	25.1	373	1	GLNA_MOUSE	P15105 mus musculus
43	44	25.1	409	1	RFL_METKA	O8xkb5 methanopyru
44	44	25.1	499	1	GLPK_XYLFA	O9p076 xyella tis
45	44	25.1	562	1	TR2M_PANAY	Q47861 pantocoe agg

ALIGNMENTS

RESULT 1	SDPL_MOUSE	STANDARD;	PRT;	89 AA.
AC	P40224:			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating factor) (TISF).			
DE	factor) (TISF).			
GN	CXCL12 OR SDF1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94181581; PubMed=8134392;			
RA	Nagasawa T., Kikutani H., Kishimoto T.;			
RT	"Molecular cloning and structure of a pre-B-cell growth-stimulating factor.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93342488; PubMed=8342023;			
RA	Tashiro K., Tada H., Heikler R., Shirozu M., Nakano T., Horjo T.;			
RT	"Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins.";			
RL	Science 261:600-603(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95073497; PubMed=7982471;			
RA	Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,			
RT	Weinstein I.B.,			
RL	"Molecular cloning of TPAP1, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";			
Exp. Cell Res.	215:284-293(1994).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-AKR/J;			
RA	Nomura M., Narata Y., Uzuwa A., Nose M., Akashi M., Suzuki G.;			
RL	Submitted (Dec-1994) to the EMBL/Genbank/DBS databases.			
CC	-1- FUNCTION: CHEMOKINE/ATTRACTION ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT NOT NEUTROPHILS.			
CC	-1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE STROMAL CELL-DEPENDENT B-CELL CLONE DW34 CELLS.			
CC	-1- ALTERNATIVE PRODUCTS: Named isoforms=2;			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=Alpha;			
CC	Isoid=P40224-1; Sequence=Displayed;			
CC	Name=Beta;			
CC	Isoid=P40224-2; Sequence=VSP_001057;			
CC	-1- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).			

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D21072; BAA04648.1; -
DR EMBL: L12029; AAA40100.1; -
DR EMBL: L12030; AAA40101.1; -
DR EMBL: S74318; AAB32650.1; -
DR EMBL: D43804; BAA07862.1; -
DR EMBL: D43805; BAA07863.1; -
DR PIR: A53497; A53497.
DR PIR: I81182; I81182.
DR HSSP: P48061; ISDF.
DR MGD: MGI103556; CXCL12.
DR GO: GO:0008009; F:chemokine activity; IDA.
DR GO: GO:0007420; P:brain development; IDA.
DR GO: GO:0030334; P:regulation of cell migration; IDA.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL12; CXCL12.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00189; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
DR Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
DR SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 55 BY SIMILARITY.
FT DISULFID 32 71 BY SIMILARITY.
FT VARSPLIC 89 89 K -> KRUKM (in isoform Beta).
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E557A CRC64;
Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 3,4e-10;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
QY 1 KPVSLSYRCPREFSG-----GGLKWTIOE 24
DB 22 KPVSLSYRCPREFSHARANKHLKILTPNCALQIVARLKNNNROYCIDPKLWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

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CC -----
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name-Beta;
CC IsoId=062657-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=062657-2; Sequence=VSP_001055;
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
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CC -----
DR EMBL: AB011966; BAA28602.1; -
DR HSSP: P48061; ISDF.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL12; CXCL12.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00189; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
DR Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
DR SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 55 BY SIMILARITY.
FT DISULFID 32 71 BY SIMILARITY.
FT VARSPLIC 90 93 MISSING (in isoform Alpha).
SQ SEQUENCE 93 AA; 10581 MW; 44FC763711E9B37 CRC64;
Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 3,6e-10;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
QY 1 KPVSLSYRCPREFSG-----GGLKWTIOE 24
DB 22 KPVSLSYRCPREFSHARANKHLKILTPNCALQIVARLKNNNROYCIDPKLWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

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RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=LIVER;
 RA Begun N.A., Barnard G.F.;
 RT "Nucleotide sequence of hIRH, human interleukin reduced in
 RT hepatomas.";
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP STRUCTURE BY NMR OF 22-88.
 RX MEDLINE=98046030; PubMed=9384579;
 RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Anara A.,
 RA Arenzana-Seisdedos F., Vitellier J.L., Baggiolini M., Sykes B.D.,
 RA Clark-Lewis I.;
 RT "Solution structure and basis for functional activity of stromal
 RT cell-derived factor-1; dissociation of CXCR4 activation from binding
 RT and inhibition of HIV-1.";
 RL EMBL J. 16:6996-7007(1997).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
 RX MEDLINE=98284037; PubMed=9618518;
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
 RA Ioliss E.;
 RT "Crystal structure of chemically synthesized [N3A] stromal
 RT cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
 RT coreceptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998)
 CC -1- FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 CC NOT NEUTROPHILS.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Beta;
 CC IsoId=P48061-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=P48061-2; Sequence=VSP_001056;
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
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 CC -----
 DR EMBL: U16752; AAA97434.1; -;
 DR EMBL: L36033; AAB39332.1; -;
 DR EMBL: L36034; AAB39333.1; -;
 DR EMBL: U19495; AAB40516.1; -;
 DR PIR: G01540; G01540.
 DR PDB: 1SDF; 28-JAN-98.
 DR PDB: 2SDF; 17-JUN-98.
 DR PDB: 1A15; 12-AUG-98.
 DR PDB: 1OG7; 28-FEB-01.
 DR GeneW; HGNC:10672; CXCL12.
 DR MIM; 600835; -;
 DR GO: GO:0003800; F:antiviral response protein activity; TAS.
 DR GO: GO:0008009; F:chemokine activity; TAS.
 DR GO: GO:0006874; P:calcium ion homeostasis; TAS.
 DR GO: GO:0007155; P:cell adhesion; TAS.
 DR GO: GO:0006935; P:chemotaxis; TAS.
 DR GO: GO:0008015; P:circulation; TAS.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR GO: GO:0006955; P:immune response; TAS.
 DR GO: GO:0008064; P:regulation of actin polymerization and/or d. . .; TAS.
 DR GO: GO:0006915; P:response to viruses; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR001089; CXCL12.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCV; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
 KW 3d-structure.

FT SIGNAL 1 19
 FT CHAIN 20 93
 FT DISULFID 30 55
 FT DISULFID 32 71
 FT VARSPLIC 90 93
 FT
 FT STRAND 36 36
 FT HELIX 41 43
 FT STRAND 44 52
 FT STRAND 53 55
 FT STRAND 56 63
 FT TURN 64 66
 FT TURN 69 72
 FT TURN 74 75
 FT HELIX 77 85
 FT TURN 86 87
 SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44F8D CRC64;
 Query Match 66.9%; Score 117; DB 1; Length 93;
 Best Local Similarity 40.3%; Pred. No. 3.6e-10;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
 QY 1 KPVSLSYRCPCHFFEG-
 DB 22 KPVSLSYRCPCHFFESHARAVKHLKIINTPCALQIVARLKNRRQVCIDPKLKWIOE 81
 QY 25 YLEKALN 31
 DB 82 YLEKALN 88
 RESULT 4
 CEFD_STRCL STANDARD; PRT; 397 AA.
 AC P18549;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Isopenicillin N epimerase (EC 5.1.1.17).
 GN CEFD.
 OS Streptomyces clavuligerus.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycetales; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxId=1901;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
 RX MEDLINE=90299822; PubMed=164525;
 RA Kovacevic S., Tobin M.B., Miller J.R.;
 RT "The beta-lactam biosynthesis genes for isopenicillin N epimerase and
 RT deacetoxycephalosporin C synthetase are expressed from a single
 RT transcript in Streptomyces clavuligerus.";
 RL J. Bacteriol. 172:3952-3958(1990).
 RN [2]
 RP SEQUENCE OF 1-23.
 RX MEDLINE=90028393; PubMed=2804141;
 RA Usui S., Yu C.Y.A.;
 RT "Purification and properties of isopenicillin N epimerase from
 RT Streptomyces clavuligerus.";
 RL Biochim. Biophys. Acta 999:78-85(1989).
 CC -1- FUNCTION: Catalyzes the reversible isomerization between
 CC isopenicillin N and penicillin N.
 CC -1- CATALYTIC ACTIVITY: Isopenicillin N = penicillin N.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Cephalosporin antibiotics biosynthesis.
 CC -1- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
 CC aminotransferases.
 CC -----
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 CC -----
 DR EMBL: M32324: AAA26714.1: -
 DR PIR: T52311: T52311.
 DR InterPro: IPR000192: Aminotransf.
 DR Pfam: PF00286: aminotran_5; 1.
 DR PROSITE: PS00595: AA_TRANSF_CLASS_5; 1.
 KM Antibiotic biosynthesis; Isomerase; Pyridoxal phosphate.
 FT INT MET 0
 FT BINDING 215 215 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 397 AA: 43366 MW: A152741899F192FF CRC64;
 Query Match 30.9%; Score 54; DB 1; Length 397;
 Best Local Similarity 53.3%; Pred. No. 2.3;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 8 RCPDRFPGGGLKMI 22
 Db 204 RIPCDFRAGSGHKWL 218
 RESULT 5
 33A4_RABIT
 ID B3A4_RABIT STANDARD; PRT; 955 AA.
 AC O9GKY1: O9GKY2:
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Anion exchange protein 4 (Anion exchanger 4).
 GN SLC4A9 OR AE4.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND
 RP CHARACTERIZATION.
 RC TISSUE=Kidney;
 RX MEDLINE=21269379; PubMed=11102437;
 RA Tsuganezawa H., Kobayashi K., Iyori M., Araki T., Koizumi A.,
 RA Watanabe S.-I., Kaneko A., Fukao T., Yoshida T., Kim D.K.,
 RA Kanai Y., Endou H., Hayashi M., Saita T.,
 RT "A new member of the HCO3--transporter superfamily is an apical anion
 RL J. Biol. Chem. 276:8180-8189(2001).
 CC -1- FUNCTION: Probable apical anion exchanger of the beta-intercalated
 CC cells of kidney. May participate in HCO3(-) secretion.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. In contrast to
 CC the rat ortholog, it is present on apical membrane of cortical
 CC kidney cells.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative Splicing; Named isoforms=2;
 CC Name=1; Synonyms=AE4a;
 CC IsoId=O9GKY1-1; Sequence=Displayed;
 CC Name=2; Synonyms=AE4b;
 CC IsoId=O9GKY1-2; Sequence=VSP_007088;
 CC -1- TISSUE SPECIFICITY: Highly expressed in kidney. Expressed in
 CC certain types of cells in the kidney cortex.
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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 CC -----
 DR EMBL: AB038263: BAB18935.1: -
 DR EMBL: AB038264: BAB18936.1: -
 DR HSP: P02730: IBMX.
 DR InterPro: IPR001717: Anion_exchanger.

DR InterPro: IPR003020: HCO3_cotransp.
 DR Pfam: PF00955: HCO3_cotransp. 1.
 DR PRINTS: PR01211: HCO3TRANSPORT.
 DR TIGRFAMs: TIGR00834; ae; 1.
 KM Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
 FT DOMAIN 1 386
 FT TRANSMEM 387 955
 FT TRANSMEM 387 407
 FT TRANSMEM 415 435
 FT TRANSMEM 438 458
 FT TRANSMEM 472 492
 FT TRANSMEM 503 523
 FT TRANSMEM 524 595
 FT TRANSMEM 596 616
 FT TRANSMEM 637 657
 FT TRANSMEM 658 683
 FT TRANSMEM 684 704
 FT TRANSMEM 730 750
 FT TRANSMEM 785 804
 FT TRANSMEM 847 867
 FT TRANSMEM 871 891
 FT CARBOHYD 548 548
 FT CARBOHYD 572 572
 FT VARSPLIC 317 332
 SQ SEQUENCE 955 AA: 105032 MW: 04E595A2BFCA15B7 CRC64;
 Query Match 30.9%; Score 54; DB 1; Length 955;
 Best Local Similarity 55.6%; Pred. No. 5.4;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KPVSLYRCPDRFPGG 18
 Db 530 RPSLIAYGGLCGPFGG 547
 RESULT 6
 ID DAT_HAEIN STANDARD; PRT; 454 AA.
 AC P44951:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Diaminobutyrate--2-oxoglutarate aminobutyrate (EC 2.6.1.76) (L-
 DE diaminobutyrate--2-oxoglutarate aminobutyrate) (DABA
 DE aminobutyrate) (DABA-AT) (L-2,4-diaminobutyrate:2-ketoglutarate 4-
 DE aminotransferase).
 GN DAT OR H10949.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 CX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shrivley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uettermann T.R., Hanna M.C., Nguyen D.T., Saeed D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP CHARACTERIZATION. PubMed=9514614;
 RX MEDLINE=98173550;
 RA Kai H., Yamamoto S.;

RT "Two genes involved in the 1,3-diaminopropane production pathway in
 RL Haemophilus influenzae";
 CC Biol. Pharm. Bull. 21:170-173(1998).
 CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-
 CC glutamate + L-aspartic 4-semialdehyde.
 CC -1- COFACTOR: Pyridoxal phosphate (potential).
 CC -1- PATHWAY: 1,3-diaminopropane biosynthesis.
 CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
 CC aminotransferases.
 CC -----
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 CC -----
 CC EMBL: U32776; AAC22610.1; -
 CC PIR: C6104; C64104.
 CC HSSP: P12995; 1033.
 CC TIGR: H10949; -
 CC InterPro: IPR005814; Amnitrans_3.
 CC InterPro: IPR004637; Dat.
 CC Pfam: PF00202; amnitrans_3; 1.
 CC TIGRfam: TIGR00709; dat; 1.
 CC PROSITE: PS00600; AA_TRANSFERRER_CLASS_3; 1.
 CC Transferrase; Amnitransferrase; Pyridoxal phosphate; Complete proteome.
 CC BINDING 287 287 PYRIDOXAL PHOSPHATE (POTENTIAL).
 CC SEQUENCE 454 AA; 49368 MW; B4B263BA7C55063 CRC64;
 SQ
 Query Match 30.3%; Score 53; DB 1; Length 454;
 Best Local Similarity 38.5%; Pred. No. 3.6;
 Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
 2 PVSLSYRCPCFFGGGLKWIQYLE 27
 Db 181 PIPHYRCDFGIGGAGAKAYQYFE 206
 RESULT 7
 RHB_A_RHME STANDARD; PRT; 470 AA.
 ID RHB_A_RHME
 AC 0923R2;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Diaminobutyrate-2-oxoglutarate amnitransferrase (EC 2.6.1.76) (L-
 DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase) (DABA
 DE amnitransferrase) (DABA-AT) (L-2,4-diaminobutyrate:2-ketoglutarate 4-
 DE amnitransferrase).
 GN RHB_A OR RHB_A OR BA1258 OR SWA2400.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plantae; PSYMA (megaplasma 1).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RCR2011 / SU47;
 RX MEDLINE=21172875; PubMed=11274118;
 RA Lynch D., O'Brien J., Welch T., Clarke P., Cui P.O., Croso J.H.,
 RA O'Connell M.;
 RA "Genetic organization of the region encoding regulation, biosynthesis,
 RA and transport of rhizobactin 1021, a siderophore produced by
 RA Sinorhizobium meliloti";
 RT J. Bacteriol. 183:2576-2585(2001).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=1021;
 RC MEDLINE=21396509; PubMed=1181432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

RA Gurjal M., Hong A., Ruizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti psyma megaplasma";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9886(2001).
 CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-
 CC glutamate + L-aspartic 4-semialdehyde.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Rhizobactin siderophore biosynthesis.
 CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
 CC aminotransferases.
 CC -----
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 CC -----
 CC EMBL: AF110737; AAD09412.1; -
 CC PIR: B95419; B95419.
 CC PIR: T46814; T46814.
 CC HSSP: P12995; 1033.
 CC InterPro: IPR005814; Amnitrans_3.
 CC InterPro: IPR004637; Dat.
 CC Pfam: PF00202; amnitrans_3; 1.
 CC TIGRfam: TIGR00709; dat; 1.
 CC PROSITE: PS00600; AA_TRANSFERRER_CLASS_3; 1.
 CC Transferrase; Amnitransferrase; Pyridoxal phosphate; Iron transport;
 CC BINDING 304 304 PYRIDOXAL PHOSPHATE (POTENTIAL).
 CC SEQUENCE 470 AA; 50148 MW; 0377B3BB5A09049 CRC64;
 SQ
 Query Match 30.3%; Score 53; DB 1; Length 470;
 Best Local Similarity 43.8%; Pred. No. 3.8;
 Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;
 2 PVSLSYRCPCFFGGG---LKNIOEYLEKAL 30
 Db 198 PYPYRCPC---FGRGNETATLAEXFERAL 226
 RESULT 8
 PDP2_HUMAN STANDARD; PRT; 529 AA.
 ID PDP2_HUMAN
 AC 09P2J5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Pyruvate dehydrogenase [liponamide]-phosphatase 2, mitochondrial
 DE precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
 DE catalytic subunit 2) (PDP2 2).
 GN PDP2 OR KIRA1348.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.,
 RA "Prediction of the coding sequences of unidentified human genes. XVI.
 RA The complete sequences of 150 new cDNA clones from brain which code
 RA for large proteins in vitro";
 RT DNA Res. 7:65-73(2000).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932;

```

RA Strausberg R.L., Feilgenfeld E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Sherman C.M., Schler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavani T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshynsky S., Caranci P., Prange C.,
RA Rask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McManis P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schmeider A., Schein J.E., Jones S.J.W., Maira M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: CATALYZES THE DEPHOSPHORYLATION AND CONCOMITANT
CC REACTIVATION OF THE ALPHA SUBUNIT OF THE E1 COMPONENT OF THE
CC PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: [pyruvate dehydrogenase (lipoamide)] phosphate
CC + H2O = [pyruvate dehydrogenase (lipoamide)] + phosphate.
CC -1- COFACTOR: MAGNESIUM DEPENDENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A P4D PROTEIN OF
CC UNKNOWN LOCATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC -----
DR EMBL: AB037769; BAA92586.1; ALT_INIT.
DR EMBL: BC028030; AAM28030.1; -.
DR InterPro: IPR001992; PP2C-1like.
DR InterPro: IPR002022; PP2C.
DR Pfam: PF00481; PP2C; 2.
DR SMART: SMO0331; PP2C_SIG; 1.
DR SMART: SMO0332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Mitochondrion; Transf. peptide; Magnesium.
KW TRANSIT
FT TRANSIT 1 66 MITOCHONDRION (POTENTIAL)
FT CHAIN 67 529 [PROTEIN DEHYDROGENASE [LIPONAMIDE]]-
FT CHAIN 529 529 PHOSPHATASE 2.
SQ SEQUENCE 529 AA: 59978 MW: 252CAEBDAFE61A5C CRC64;
FT
QY Query Match 30.3%; Score 53; DB 1; Length 529;
Best Local Similarity 46.2%; Pred. No. 4.2;
Matches 12; Conservative 2; Mismatches 8; Indels 4; Gaps 1;
Db 344 PCRRFGGGLKTIQIE---YEKALN 31
10 PCRRFGGGLKTIQIE---YEKALN 31
ID B34A_HUMAN STANDARD: PRT, 983 AA.
AC Q96Q91; Q96RMS; Q9BXF2; Q9BXN3;
DT 15-SEP-2003 (Rel. 42; Created)
DT 15-SEP-2003 (Rel. 42; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Anion exchange protein 4 (anion exchanger 4) (Sodium bicarbonate
DE cotransporter 5).
CN S1C4A9 OR A4 OR SBC5.
OS Homo sapiens (Human).

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CC Enkayaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.
CN NOBL_TaxID=9606;
RN
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Kidney, and Testis;
RX MEDLINE=2119380; PubMed=11302728;
RA Parker M.D., Qumozdi E.P., Tanner M.J.A.;
RT "Human BRL, a new bicarbonate transporter superfamily member and
RL human AE4 from kidney.";
RN Genome Biol. 2:RESEARCH0011.1-RESEARCH0011.13(2001).
RN {3}
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Karet F.E.;
RT "Cloning and characterization of human AE4,";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN {4}
RP SEQUENCE OF 3-983 FROM N.A. (ISOFORM 3), AND TISSUE SPECIFICITY.
RC TISSUE=Testis;
RA Ishibashi K.;
RT "Molecular cloning of human sodium bicarbonate cotransporter 5,";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probable apical anion exchanger of the kidney cortex (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named Isoforms=3;
CC Name=1;
CC IsoId=Q96Q91-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96Q91-2; Sequence=VSP_007085, VSP_007086, VSP_007087;
CC Name=3;
CC IsoId=Q96Q91-3; Sequence=VSP_007085;
CC -1- TISSUE SPECIFICITY: Kidney-specific.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC
DR EMBL; AF332961; AAK69625.1; -
DR EMBL; AF336237; AAK16733.1; -
DR EMBL; AF313465; AAK28832.1; ALT_INIT.
DR EMBL; AB032762; BAA93010.1; -
DR HSSP; P02730; IBNX.
DR Genew; HGNC.11035; SLCA49.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp.1.
DR PRINTS; PR01231; HCO3TRANSPO.
DR TrEMBL; TIGR00834; ae.1.
RW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Alternative splicing.
KW Cytoplasmic (POTENTIAL).
KW Domain 1 414 MEMBRANE (ANION EXCHANGE).
FT DOMAIN 415 983 POTENTIAL.
FT TRANSMEM 445 463 POTENTIAL.
FT TRANSMEM 465 485 POTENTIAL.
FT TRANSMEM 500 520 POTENTIAL.
FT TRANSMEM 530 550 POTENTIAL.
FT TRANSMEM 552 623 POTENTIAL.
FT DOMAIN 552 623 EXOPLASMIC LOOP (POTENTIAL).

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FT TRANSMEM 624 644 POTENTIAL.
FT TRANSMEM 665 685 POTENTIAL.
FT DOMAIN 686 711 CTROPLASMIC (POTENTIAL).
FT TRANSMEM 712 732 POTENTIAL.
FT TRANSMEM 738 778 POTENTIAL.
FT TRANSMEM 815 835 POTENTIAL.
FT TRANSMEM 837 857 POTENTIAL.
FT TRANSMEM 899 919 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 600 600 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 77 100 /FTID-VSP.007085.
FT VARSPLIC 384 394 Missing (in isoform 2).
FT VARSPLIC 592 594 /FTID-VSP.007086.
FT VARSPLIC 101 101 /FTID-VSP.007087.
FT CONFLICT 453 453 R -> T (IN REF. 3).
FT CONFLICT 795 795 V -> M (IN REF. 1).
FT CONFLICT 795 795 R -> K (IN REF. 1).
SQ SEQUENCE 983 AA; 108247 MW; E2ABD4C9D275B6C CRC64;

Query Match 29.7%; Score 52; DB 1; Length 983;
Best Local Similarity 44.0%; Pred. No. 11;
Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 1 KPVSLSRCPGCRFFGGG--LKWIQ 23
Db 558 KPGSSAYGCLQYPPGNGESQWIR 582

RESULT 10
HXCC_HUMAN STANDARD; PRT; 282 AA.
ID HXCC_HUMAN
AC P31275; Q9BX16;
DT 01-JUL-1993 (Rel. 26, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C12 (Hox-3f).
GN HoxC12 or Hox3f.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kosaki K., Kosaki R., Suzuki T., Yoshinashi H., Sasaki K., Matsuo N.;
RT "A complete mutation analysis panel of human HOX genes.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 214-279 FROM N.A.
RP MEDLINE=90098876; PubMed=2574852;
RA Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio E.,
RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;
RT "The human HOX gene family.";
RL Nucleic Acids Res. 17:10385-10402(1989)
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SIMILARITY: BELONGS TO THE ABD-B HOMEBOX FAMILY.
CC -----
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CC -----
DR EMBL; AF328962; AAK16717.1;
DR EMBL; AF328963; AAK16717.1; JOINED.
DR PIR; S14933; S14933.
DR HSP; P14653; I872.

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DR TRANSFAC; T03329;
DR Genem; HGNC:5124; HOXC12.
DR MIM; 142975;
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox.1.
DR PRINTS; PR00024; HOMEBOX.
DR Prodom; PD00010; Homeobox.1.
DR SMART; SM00389; HOX.1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00711; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DNA_BIND 214 273 HOMEBOX.
SQ SEQUENCE 282 AA; 30171 MW; 493C53C511054AD CRC64;

Query Match 29.1%; Score 51; DB 1; Length 282;
Best Local Similarity 37.8%; Pred. No. 4.5;
Matches 14; Conservative 1; Mismatches 4; Indels 18; Gaps 1;

QY 2 PVSLS-----YRCPGRFFGGGGLK 20
Db 72 PVSLSNPPRGTCALARVEDGKGYREPCAGGGGGLK 108

RESULT 11
PDP2_RAT STANDARD; PRT; 530 AA.
ID PDP2_RAT
AC O88484;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE [Pyruvate dehydrogenase (lipoamide)]-phosphatase 2, mitochondrial
DE precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
DE catalytic subunit 2) (PDP 2).
GN PDP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98316337; PubMed=9651365;
RA Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;
RT "Isoenzymes of pyruvate dehydrogenase phosphatase. DNA-derived amino
RT acid sequences, expression, and regulation.";
RL J. Biol. Chem. 273:17680-17688(1998).
CC -1- FUNCTION: CATALYZES THE DEPHOSPHORYLATION AND CONCOMITANT
CC REACTIVATION OF THE ALPHA SUBUNIT OF THE E1 COMPONENT OF THE
CC PYRUVATE DEHYDROGENASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipoamide)] phosphate
CC + H(2)O = [pyruvate dehydrogenase (lipoamide)] + phosphate.
CC -1- COFACTOR: MAGNESIUM.
CC -1- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A P2C PROTEIN OF
CC UNKNOWN FUNCTION (BY SIMILARITY).
CC -1- UNKNOWN FUNCTION LOCATION: Mitochondrial matrix.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER.
CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
CC -----
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CC -----
DR EMBL; AF062741; AAC40168.1;
DR InterPro; IPR001932; P2C-1like.
DR Pfam; PF00481; P2C; 2.
DR SMART; SM00331; P2C-SIG; 1.
DR SMART; SM00332; P2CC; 1.

```

DR PROSITE: PS01032; PP2C; 1.
 KW Hydrolyase; Mitochondrion; Transit peptide; Magnesium.
 FT TRANSIT 1 67 MITOCHONDRION (POTENTIAL).
 FT CHAIN 68 530 [PYRUVATE DEHYDROGENASE (LIPONMIDE)]-
 FT SEQUENCE 530 AA; 59654 MW; 5AB688FAC78AD9CD CRC64;
 PHOSPHATASE 2.
 Query Match 28.6%; Score 50; DB 1; Length 530;
 Best Local Similarity 47.6%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
 OY 10 PCRFGGGGLKMWIELEKAL 30
 DB 345 PCRAFQDVQKMKSKELQNRNL 365

RESULT 12
 GLPK_MYCLE STANDARD; PRT; 508 AA.
 AC 09C81;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
 GN GLPK OR ML2314.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Elismeler K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltingworth T., Fraser A., Hamlin N.,
 RA Holtroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND
 METABOLISM.
 CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
 CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
 CC -1- SIMILARITY: BELONGS TO THE FOCOKINASE / GLUCOKINASE /
 GLYCEROKINASE / XYLOKINASE FAMILY.
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 CC
 CC EMBL: AL583925; CAC31830.1; -
 DR PIR: F87198; F87198.
 DR HSSP: P08859; IGIC.
 DR Leproma; ML2314; -
 DR HAMAP: MF_00186; -; 1.
 DR InterPro: IPR000577; FGGY_Kin.
 DR InterPro: IPR005999; Glycerol_Kin.
 DR Pfam: PF02782; FGGY_C.1.
 DR Pfam: PF02782; FGGY_C.1.
 DR TIGR: TIGR01311; glycerol_kin; 1.
 DR PROSITE: PS00933; FGGY_KINASES_1; 1.
 DR PROSITE: PS00445; FGGY_KINASES_2; 1.
 KW Glycerol metabolism; Transferase; Kinase; ATP-binding;

KW Complete proteome. 168 ATP (PROBABE).
 FT NP_BIND 156
 FT SEQUENCE 508 AA; 54658 MW; A153797933ECFA039 CRC64;
 SQ
 Query Match 28.0%; Score 49; DB 1; Length 508;
 Best Local Similarity 44.4%; Pred. No. 16;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 10 PCRFGGGGLKMWIELEKAL 27
 DB 134 PATVSGGKLQMLENV 151

RESULT 13
 GLPK_MYCTU STANDARD; PRT; 517 AA.
 AC 06966;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
 GN GLPK OR RV3696C OR MT3798 OR MTV025.044C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Elismeler K., Gas S., Barry C.E. III, Tekela F.,
 RA Baccocck K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltingworth T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Kirogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultison J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND
 METABOLISM.
 CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
 CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
 CC -1- SIMILARITY: BELONGS TO THE FOCOKINASE / GLUCOKINASE /
 GLYCEROKINASE / XYLOKINASE FAMILY.
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 CC
 CC EMBL: AL022121; CAA18018.1; -
 DR PIR: A70793; A70793.
 DR HSSP: P08859; IGIC.
 DR TIGR: MT3798; -;


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DR Tuberculin; RV3696C;
DR HAMAP; MF_00186; 1.
DR InterPro: IPR000577; FG_Y_Kin.
DR InterPro: IPR005999; Glycerol_Kin.
DR Pfam: PF00370; FG_Y_1.
DR Pfam: PF02782; FG_Y_C; 1.
DR TIGRfam: TIGR01311; glycerol_kin.1.
DR PROSITE: PS00445; FG_Y_KINASES_2; 1.
DR PROSITE: PS00933; FG_Y_KINASES_1; 1.
DR Glycerol metabolism; Transferase; Kinase; ATP-binding;
KW Complete proteome.
FT NP_BIND 165 177 ATP (PROBABLE);
SQ SEQUENCE 517 AA; 55859 MW; 7E3F30DCF2A1E63E CRC64;

Query Match
Best Local Similarity 28.0%; Score 49; DB 1; Length 517;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 10 PCRFGGGGLKMIQYLEK 27
DB 143 PATYFGGKLMLEND 160

RESULT 14
TRZM_PSSS STANDARD; PRT; 557 AA.
ID TRZM_PSSS
AC P06617;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN IAM
OS Pseudomonas syringae (pv. savastanoi).
OG Plasmid pIAM.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=29438;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EW2009;
RA Yamada T., Palm C.J., Brooks B., Kosuge T.;
RT Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid
RL genes show homology with Agrobacterium tumefaciens T-DNA.;
RL Proc. Natl. Acad. Sci. U.S.A. 82:6522-6526(1985).
-1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CO(2) + H(2)O.
CC -1- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
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CC EMBL: M11035; AAA35852.1;
DR PIR: A25493; A25493;
DR InterPro: IPR000759; Adnrx_reductase.
DR InterPro: IPR002937; Amino_oxidase.
DR Pfam: PF01593; Amino_oxidase; 1.
DR PRINTS: PR00419; ADXRDTASE.
KW Plasmid; Oxidoreductase; Monooxygenase; Auxin biosynthesis.
SQ SEQUENCE 557 AA; 61861 MW; A3EASCF7BA94289 CRC64;

Query Match
Best Local Similarity 28.0%; Score 49; DB 1; Length 557;
Matches 10; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 9 CPCRFGGGGLKMIQYLEKALN 31
DB 511 CSCSFAGG---WIEGAVOTALN 529

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RESULT 15
YP3_CAEEL STANDARD; PRT; 1714 AA.
ID YP3_CAEEL
AC C09475;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative helicase C28H8.3 (EC 3.6.1.-).
GN C28H8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N., Waterston R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
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CC
CC EMBL: U20861; AAA62291.2;
DR WormPepp: C28H8.3; C28H8.3;
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00480; HELIC; 1.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
KW Nuclear protein.
FT NP_BIND 607 614 ATP (POTENTIAL);
FT NP_BIND 806 813 ATP (POTENTIAL);
FT SITE 913 916 DEVH BOX.
SQ SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;

Query Match
Best Local Similarity 28.0%; Score 49; DB 1; Length 1714;
Matches 13; Conservative 1; Mismatches 7; Indels 6; Gaps 2;

QY 10 PCRFGGGGLK--MIQ-----EYLEKAL 30
DB 1058 PCRFGGGGLKAWISRELRLENAL 1084

Search completed: October 9, 2003, 09:18:15
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:42 ; Search time 95 Seconds

(without alignments)
84.207 Million cell updates/sec

Title: US-09-835-107a-11

Perfect score: 175

Sequence: 1 KPVSLSYRCPCRFEGGGLKWIQIELEKALN 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	117	66.9	89	6 Q8HYPO	Q8HYPO macaca mula
2	117	66.9	92	4 Q9H554	Q9H554 homo sapien
3	114	65.1	89	11 Q9QZD1	Q9QZD1 rattus norv
4	105	60.0	94	13 Q8UJ9	Q8UJ9 xenopus lae
5	61	34.9	108	10 Q48947	Q48947 arabidopsi
6	61	34.9	108	10 Q9S322	Q9S322 arabidopsi
7	61	34.9	974	10 P93155	P93155 gossypium h
8	60.5	34.6	974	10 Q8W1M0	Q8W1M0 gossypium h
9	60.5	34.6	974	10 Q8L778	Q8L778 arabidopsi
10	58	33.1	366	10 Q94U06	Q94U06 pseudomonas
11	58	33.1	1069	10 Q9F1B9	Q9F1B9 arabidopsi
12	58	33.1	1081	10 Q65338	Q65338 arabidopsi
13	58	33.1	1084	10 Q9FGP9	Q9FGP9 arabidopsi
14	58	33.1	1084	10 Q943H3	Q943H3 oryza sativ
15	57.5	32.9	939	10 Q943H3	Q943H3 oryza sativ

17	57	32.6	153	16 Q8FKT6	Q8FKT6 escherichia
18	57	32.6	424	5 Q9VCS4	Q9VCS4 drosophila
19	56.5	32.3	978	10 Q81368	Q81368 populus tre
20	56	32.0	233	16 Q86804	Q86804 streptomyces
21	54	30.9	422	5 Q9GUF1	Q9GUF1 caenorhabdi
22	54	30.9	939	6 Q9GKY1	Q9GKY1 oryctolagus
23	54	30.9	955	6 Q9GKY2	Q9GKY2 oryctolagus
24	53.5	30.6	99	13 Q8AV10	Q8AV10 brachydanio
25	52.5	30.0	141	4 Q8N796	Q8N796 homo sapien
26	52	29.7	220	5 Q8T4G9	Q8T4G9 drosophila
27	52	29.7	945	4 Q9H4F2	Q9H4F2 homo sapien
28	52	29.7	957	4 Q9GQ91	Q9GQ91 homo sapien
29	52	29.7	959	4 Q9GRM5	Q9GRM5 homo sapien
30	52	29.7	990	4 Q9RXN3	Q9RXN3 homo sapien
31	52	29.7	1063	10 Q9AV71	Q9AV71 oryza sativ
32	51	29.1	280	11 Q8K558	Q8K558 mus musculu
33	51	29.1	322	5 Q8S528	Q8S528 encephalito
34	51	29.1	353	5 Q9NBJ2	Q9NBJ2 drosophila
35	51	29.1	366	5 Q9NBJ1	Q9NBJ1 drosophila
36	51	29.1	959	16 Q8D8D0	Q8D8D0 vibrio vuln
37	51	29.1	1440	5 Q20204	Q20204 caenorhabdi
38	50.5	28.9	392	2 Q07470	Q07470 rhodospirillum rubrum
39	50.5	28.9	527	17 Q8PYH3	Q8PYH3 methanococcus
40	50.5	28.9	729	17 Q8T1W4	Q8T1W4 methanococcus
41	50	28.6	202	16 Q8YEH5	Q8YEH5 brucella me
42	50	28.6	202	16 Q8G3B1	Q8G3B1 brucella su
43	50	28.6	366	5 Q9NBJ3	Q9NBJ3 drosophila
44	50	28.6	685	10 P93156	P93156 gossypium h
45	49.5	28.3	170	10 Q9S0H7	Q9S0H7 arabidopsi

ALIGNMENTS

RESULT 1
Q8HYPO ID Q8HYPO PRELIMINARY: PRT: 89 AA.
AC Q8HYPO;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Chemokine CXCL12/SDF-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhsu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhardt T.A.;
RT "Comprehensive cloning and sequencing reveals evolutionary
RT conservation among all groups of rhesus macaque chemokines."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF49283; AAN76086.1; -
SQ SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;

Query Match 66.9%; Score 117; DB 6; Length 89;

Best Local Similarity 40.3%; Pred. NO. 1.5e-09; Mismatches 27; Conservative 0; Indels 4; Gaps 1;

QY	1 KPVSLSYRCPCRFEGG	-----GLKWIQIE 24
QY		
Db	22 KPVSLSYRCPCRFESHVARANKHKKIINTPCALQIVARLKNRRQVCIDPKIKWIE 81	
QY	25 YLEKALN 31	
QY		
Db	82 YLEKALN 88	

RESULT 2
Q9H554 ID Q9H554 PRELIMINARY: PRT: 92 AA.
AC Q9H554;

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DE 01-MAR-2001 (TREMBlrel. 16, Created)
DE 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)
DE (Fragment).
GN SDF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137026; CAC10202.1; -.
DR HSSP; P48061; ISDF.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
FT NON TER
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B44EBD20 CRC64;

Query Match
Best Local Similarity 40.3%; Score 117; DB 4; Length 92;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQ 24
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNRQVCIDPKWKWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 3
Q9QZD1 PRELIMINARY; PRT; 89 AA.
ID Q9QZD1
AC Q9QZD1;
DC 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-SPRAGUE-DAWLEY;
RA Ohnami Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "CDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
RT alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillarsetti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
RT alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF189724; AA01066.1; -.
DR HSSP; P48061; ISDF.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2B35FA CRC64;

Query Match
Best Local Similarity 38.8%; Score 114; DB 11; Length 89;
Matches 26; Conservative 1; Mismatches 4; Indels 36; Gaps 1;

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QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQ 24
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNRQVCIDPKWKWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 4
Q8UDJ9 PRELIMINARY; PRT; 94 AA.
ID Q8UDJ9
AC Q8UDJ9;
DC 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OX Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Spleen;
RC Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis stromal-derived factor 1: conservation of structure
RT and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278857; CAC82196.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR SIGNAL.
FT CHAIN
FT SIGNAL
FT CHAIN
SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match
Best Local Similarity 35.8%; Score 105; DB 13; Length 94;
Matches 24; Conservative 1; Mismatches 6; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQ 24
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNRQVCIDPKWKWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 5
Q93YP8 PRELIMINARY; PRT; 507 AA.
ID Q93YP8
AC Q93YP8;
DC 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Cellulose synthase catalytic subunit (Atr-A).
GN ATAG939350
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Barn J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Naitusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

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RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Bann J., Carinci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY059858; AA124340.1; -
DR EMBL: AY093308; AA13307.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR Pfam: PF03552; Cellulose_synth; 1.
SQ SEQUENCE 507 AA; 5665 MW; D0433743E31DE61 CRC64;

Query Match
Best Local Similarity 34.9%; Score 61; DB 10; Length 507;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 VSLSTPCPRFFGGGGLKWIQY 25
DB 256 IFLSRHCPIMYGCGGLKWLRF 278

RESULT 6
O48947 PRELIMINARY; PRT; 1084 AA.
ID 048947;
AC 048947;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Cellulose synthase catalytic subunit.
GN H-A OR T22F8.250 OR ATG639350.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RC MEDLINE=98111412; PubMed=9445479;
RA Arioli T., Peng L., Betzner A.S., Burn J., Wittke W., Herth W.,
RA Camilleri C., Hottel H., Plazinski J., Birch R., Cork A., Glover J.,
RA Redmond J., Williamson R.E.;
RT "Molecular analysis of cellulose biosynthesis in Arabidopsis.";
RL Science 279:717-720(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bevan M., Zimmermann W., Gruenisen A., Wambutt R., Bancroft I.,
RA Meves H.W., Mayer K.F.X., Schueller C.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Smith A., Meves H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF027173; AAC39335.1; -
DR EMBL: AL050351; CAB3650.1; -
DR EMBL: AL161585; CAB80598.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF03552; Cellulose_synth; 1.

RA SMART: SM00184; RING; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 1084 AA; 122068 MW; 2F9B22D169D734E0 CRC64;

Query Match
Best Local Similarity 34.9%; Score 61; DB 10; Length 1084;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 VSLSTPCPRFFGGGGLKWIQY 25
DB 833 IFLSRHCPIMYGCGGLKWLRF 855

RESULT 7
O9S222 PRELIMINARY; PRT; 1088 AA.
ID O9S222;
AC O9S222;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Putative cellulose synthase catalytic subunit.
GN ANG21770.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldguy T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhafer G.P., Preuss D., Niekman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RC Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC007019; AAD20396.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF03552; Cellulose_synth; 1.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 1088 AA; 123446 MW; 06057111860DDC9F CRC64;

Query Match
Best Local Similarity 34.9%; Score 61; DB 10; Length 1088;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 VSLSTPCPRFFGGGGLKWIQY 25
DB 837 IFLSRHCPIMYGCGGLKWLRF 859

RESULT 8
P93155 PRELIMINARY; PRT; 974 AA.
ID P93155;
AC P93155;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Cellulose synthase.
GN CELA1.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoidae; Gossypium.
OX NCB1_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Acata ST-2; TISSUE=Flower;
RA MEDLINE=97051296; Pubmed=6901635;
RA Pear J.R., Kawagoe Y., Schreckengost W.E., Delmer D.P., Stalker D.M.;
RT "Higher plants contain homologs of the bacterial cella genes encoding
RT the catalytic subunit of cellulose synthase."
RL Proc. Natl. Acad. Sci. U.S.A. 93:12637-12642(1996).
DR EMBL: U58283; AAB37766.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR Pfam: PF03552; Cellulose_synth.1;
SQ SEQUENCE 974 AA; 109703 MW; 2656CA2D05D100A7 CRC64;

Query Match 34.6%; Score 60.5; DB 10; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.9;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23
Db 721 IFLSRHCPIMWYGGGRLKWLQ 742

RESULT 9
O8W1W0 PRELIMINARY; PRT; 974 AA.
AC O8W1W0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cellulose synthase A4.
GN CESX4.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoidae; Gossypium.
OX NCB1_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim H.Y., Triplett B.A., PubMed=11743074;
RT Cotton Fiber Growth in planta and in vitro. Models for Plant Cell
RT Elongation and Cell Wall Biogenesis.
RT Plant Physiol. 127:1361-1366(2001).
RL EMBL: AF413210; AAL37718.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR Pfam: PF03552; Cellulose_synth.1;
SQ SEQUENCE 974 AA; 109439 MW; F8AF66ABA2B8071 CRC64;

Query Match 34.6%; Score 60.5; DB 10; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.9;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23
Db 721 IFLSRHCPIMWYGGGRLKWLQ 742

RESULT 10
O8L778 PRELIMINARY; PRT; 346 AA.
AC O8L778;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cellulose synthase catalytic subunit.
GN AT5G09870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.

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OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan Y.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shimizu P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY136423; AAM97089.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR Pfam: PF03552; Cellulose_synth.1;
SQ SEQUENCE 346 AA; 38558 MW; 80799D6E46D57090 CRC64;

Query Match 33.1%; Score 58; DB 10; Length 346;
Best Local Similarity 47.6%; Pred. No. 3;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23
Db 96 IFLSRHCPIMWYGGGRLKWLQ 116

RESULT 11
O94J06 PRELIMINARY; PRT; 366 AA.
AC O94J06;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE AT5G64740/MVF7-7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
RA Bann J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan Y.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF375439; AAK53023.1; -
DR EMBL: AY143957; AAN28896.1; -
DR InterPro: IPR005150; Cellulose_synth.
DR Pfam: PF03552; Cellulose_synth.1;
SQ SEQUENCE 366 AA; 40788 MW; A287A60060D3EE2B CRC64;

Query Match 33.1%; Score 58; DB 10; Length 366;
Best Local Similarity 47.6%; Pred. No. 3.2;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VLSYRCPCRF-FGGGGLKWIQ 23

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Db 116 IFLSRHCPITWYGCGGLKMLE 136

RESULT 12

Q91168 PRELIMINARY: PRT: 469 AA.

AC Q91168. 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Probable class III aminotransferase.
 GN PA2413.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;

Sequence from N.A.
 RC STRAIN-ATCC 15692 / PA01;
 RA MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lapidis G., Lam R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen";
 RT Nature 406:959-964(2000).
 RL EMBL: AE004668; AAC05801.1; -;
 DR HSSP: P16932; ZDRB.
 DR InterPro: IPR005814; AminoTrans_3.
 DR InterPro: IPR004637; Dat.
 DR Pfam: PF00202; aminoTrans_3; 1.
 DR TIGRPFAM: TIGR00709; dat; 1.
 DR PROSITE: PS00600; AA_TRANSFR_CLASS_3; 1.
 DR Translatase; AminoTransferase; Complete Proteome.
 KW SEQUENCE 469 AA; 50215 MW; FAAB575E8A44EE8 CRC64;

Query Match 33.1%; Score 58; DB 16; Length 469;
 Best Local Similarity 43.3%; Pred. No. 4.2;
 Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2 VSLSYRCPGCRFFGGGGLKMWIQEYLFKALN 31
 DB 199 PYPDYRCPGGLGEGVAKANLHYELNINL 228

RESULT 13

Q9FIB9 PRELIMINARY: PRT: 1069 AA.

AC Q9FIB9. 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Cellulose synthase catalytic subunit.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Columbia;
 RX MEDLINE-99156233; PubMed-10048488;
 RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
 RT Sequence features of the regions of 1,081,958 bp covered by seventeen
 RT physically assigned P1 and PAC clones.";
 RL DNA Res. 5:379-391(1998).
 DR EMBL: AB016893; BAB09408.1; -;
 DR InterPro: IPR005150; Cellulose_synt.

DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF03552; Cellulose_synt; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 SQ SEQUENCE 1069 AA; 120861 MW; D03ED5C578DB3E7C CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1069;
 Best Local Similarity 47.6%; Pred. No. 9.9;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPGCRFFGGGGLKMWIQ 23
 Db 819 IFLSRHCPITWYGCGGLKMLE 839

RESULT 14

Q65338 PRELIMINARY: PRT: 1081 AA.

AC Q65338. 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Cellulose synthase (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. Columbia.
 RA Wu L., Joshi C.P., Chiang V.L.;
 RT "Arabidopsis, a new member of the cellulose synthase gene family from
 RT Arabidopsis (Accession No. AF062485) (PGR8-114).";
 RL Plant Physiol. 117:1125-1125(1998).
 DR EMBL: AF062485; AAC29067.1; -;
 DR InterPro: IPR005150; Cellulose_synt.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF03552; Cellulose_synt; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR NON-TER
 SQ SEQUENCE 1081 AA; 122446 MW; DC59A35A1713FD9F CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 10;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPGCRFFGGGGLKMWIQ 23
 Db 831 IFLSRHCPITWYGCGGLKMLE 851

RESULT 15

Q9EGF9 PRELIMINARY: PRT: 1084 AA.

AC Q9EGF9. 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Cellulose synthase catalytic subunit.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Columbia;
 RX Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI";
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AB025637; BAB10307.1; -;
 DR InterPro; IPR005150; Cellulose_synt.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF03552; Cellulose_synt; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00089; 2F_RING_2; 1.
 SQ SEQUENCE 1084 AA; 122501 MW; 1520439A5053608C CRC64;

Query Match 33.18; Score 58; DB 10; Length 1084;
 Best Local Similarity 47.68; Pred. No. 10;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRQPCRFEGGGIKWIO 23
 :|||:|||||:
 Db 834 IFLSRHCPWYGYGGGLKWL 854

Search completed: October 9, 2003, 09:20:47
 Job time : 100 secs

Thu Oct 9 16:39:00 2003

us-09-835-107a-11.rai

Page 1

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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:46 : Search time 29 Seconds
(without alignments)
45.229 Million cell updates/sec

Title: US-09-835-107A-11

Sequence: 1 KPVLSYRCPCRFGGGLKMWIYELKALN 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCRTUS.COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/Backfilest.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	1	US-08-181-556-2
2	117	66.9	89	1	US-08-323-084A-1
3	117	66.9	89	1	US-08-674-008-1
4	117	66.9	93	1	US-08-323-084A-5
5	117	66.9	93	1	US-08-674-008-5
6	117	66.9	93	4	US-09-312-283C-421
7	117	66.9	166	4	US-09-646-028-5
8	117	66.9	177	4	US-09-646-028-54
9	117	66.9	326	3	US-08-808-720-3
10	117	66.9	328	3	US-08-808-720-1
11	117	66.9	339	4	US-09-646-028-55
12	117	66.9	1084	4	US-09-221-013A-8
13	60.5	34.6	974	3	US-08-960-048-6
14	60.5	34.6	974	4	US-09-838-586-6
15	58	33.1	535	4	US-09-252-991A-26662
16	50	28.6	588	3	US-08-481-190-16
17	50	28.6	588	5	PCT-US93-00869-16
18	50	28.6	685	5	US-08-960-048-7
19	50	28.6	685	4	US-09-838-586-7
20	49.5	28.3	504	4	US-09-252-991A-32272
21	49	28.0	416	1	US-08-117-083-61
22	49	28.0	488	4	US-08-311-731A-23
23	48	27.4	78	3	US-09-188-930-158
24	48	27.4	78	3	US-09-188-930-158
25	48	27.4	78	4	US-09-312-283C-158
26	48	27.4	78	4	US-09-312-283C-285
27	48	27.4	125	3	US-08-722-126A-7

28	48	27.4	125	5	PCT-US93-04258-7	Sequence 7, Appli
29	48	27.4	287	1	US-08-365-103B-4	Sequence 4, Appli
30	48	27.4	300	1	US-08-365-103B-6	Sequence 6, Appli
31	48	27.4	327	1	US-08-365-103B-2	Sequence 2, Appli
32	48	27.4	560	4	US-09-252-991A-30180	Sequence 30180, A
33	47.5	27.1	305	4	US-09-252-991A-26204	Sequence 26204, A
34	46	26.3	186	1	US-08-089-458B-6	Sequence 6, Appli
35	46	26.3	455	6	5168051-11	Patent No. 5168051
36	45	25.7	927	4	US-09-252-991A-20340	Sequence 20340, A
37	45	25.7	173	4	US-09-252-991A-32359	Sequence 32359, A
38	45	25.7	252	2	US-08-198-452A-1215	Sequence 1215, Ap
39	45	25.7	292	2	US-08-701-191A-40	Sequence 40, Appl
40	45	25.7	514	4	US-09-266-965-114	Sequence 114, App
41	45	25.7	581	1	US-08-446-038B-17	Sequence 17, Appl
42	45	25.7	581	1	US-08-446-010B-17	Sequence 17, Appl
43	45	25.7	581	2	US-08-805-445-17	Sequence 17, Appl
44	45	25.7	581	2	US-08-064-067D-17	Sequence 17, Appl
45	45	25.7	581	2	US-09-066-208-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-181-556-2
Sequence 2, Application US/08181556
Patent No. 5525486
GENERAL INFORMATION:
APPLICANT: HONJO, Tasaku
APPLICANT: TASHIRO, Kei
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING cDNA LIBRARY,
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND DNA CODING FOR THE SAME
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER
STREET: 515 No. 5525486th Washington Street (P.O. Box 1427)
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22312
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,556
FILING DATE: 14-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-22098
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, James A.
REGISTRATION NUMBER: 31714
REFERENCE/DOCKET NUMBER: TTP/29088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-7200
TELEFAX: (703) 528-5313
TELEX: 89-2746
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-181-556-2
Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 6.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
|||||
Db 22 KPVSLSYRCPCRFEGGSHVAVANVKKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 81
QY 25 YLEKALN 31
|||||
Db 82 YLEKALN 88

RESULT 2
US-08-323-084A-1
Sequence 1, Application US/08323084A
Patent No. 5563048
GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,084A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-084A-1

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 6.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
|||||
Db 22 KPVSLSYRCPCRFEGGSHVAVANVKKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 81
QY 25 YLEKALN 31
|||||
Db 82 YLEKALN 88

RESULT 3
US-08-674-008-1
Sequence 1, Application US/08674008
Patent No. 5756084
GENERAL INFORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
FACTOR 1 AND 1 (As Amended)

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-008-1

Query Match 66.9%; Score 117; DB 1; Length 89;
Best Local Similarity 40.3%; Pred. No. 6.6e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
|||||
Db 22 KPVSLSYRCPCRFEGGSHVAVANVKKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 81
QY 25 YLEKALN 31
|||||
Db 82 YLEKALN 88

RESULT 4
US-08-323-084A-5
Sequence 5, Application US/08323084A
Patent No. 5563048
GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,084A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-084A-5

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.9e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
DB 22 KPVSLSYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 5
US-08-674-008-5
Sequence 5, Application US/08674008
Patent No. 5756084
GENERAL INFORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
TITLE OF INVENTION: FACTOR 1 AND 1 (As Amended)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRU, MICHAEL, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-008-5

Query Match 66.9%; Score 117; DB 1; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.9e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
DB 22 KPVSLSYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 6
US-09-312-283C-421
Sequence 421, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Oarust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated from skin cells
TITLE OF INVENTION: and Methods for their use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 421
LENGTH: 93
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-421

Query Match 66.9%; Score 117; DB 4; Length 93;
Best Local Similarity 40.3%; Pred. No. 6.9e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIOE 24
DB 22 KPVSLSYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 7
US-09-646-028-5
Sequence 5, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arty
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 166
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-5

Query Match 66.9%; Score 117; DB 4; Length 166;
Best Local Similarity 40.3%; Pred. No. 1.2e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQ 24
DB 22 KPVSLSYRCPCRFEGGSHVAVANVHKILNTPNCALQIVARLKNNNROVCIDPKLWIOE 81
QY 25 YLEKALN 31
DB 82 YLEKALN 88

RESULT 8

US-09-646-028-54
Sequence 54, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Bitagyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIORITY FILING DATE: 1998-03-12
PRIORITY FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 54
LENGTH: 177
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Artificial Sequence
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-54

Query Match 66.9%; Score 117; DB 4; Length 177;
Best Local Similarity 40.3%; Pred. No. 1.3e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQ 24
DB 4 KPVSLSYRCPCRFEGGSHVAVANVHKILNTPNCALQIVARLKNNNROVCIDPKLWIOE 63
QY 25 YLEKALN 31
DB 64 YLEKALN 70

RESULT 9

US-08-808-720-3
Sequence 3, Application US/08808720
Patent No. 6100387
GENERAL INFORMATION:
APPLICANT: Hermann, Steve
APPLICANT: Swandberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-720-3

Query Match 66.9%; Score 117; DB 3; Length 326;
Best Local Similarity 40.3%; Pred. No. 2.5e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQ 24
DB 20 KPVSLSYRCPCRFEGGSHVAVANVHKILNTPNCALQIVARLKNNNROVCIDPKLWIOE 79
QY 25 YLEKALN 31
DB 80 YLEKALN 86

RESULT 10

US-08-808-720-1
Sequence 1, Application US/08808720
Patent No. 6100387
GENERAL INFORMATION:
APPLICANT: Hermann, Steve
APPLICANT: Swandberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-808-720-1

Query Match 66.9%; Score 117; DB 3; Length 328;
Best Local Similarity 40.3%; Pred. No. 2.5e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQE 24
|||
Db 22 KPVSLSYRCPCRFESHVARANKHLKLTNPVCAQIVARLKNNNRQYCIDPKLWQE 81
|||

QY 25 YLEKALN 31
|||
Db 82 YLEKALN 88

RESULT 11

US-09-646-028-55
Sequence 55, Application US/09646028
Patent No. 6562347

GENERAL INFORMATION:
APPLICANT: Kwak, Larry

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028

CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55

LENGTH: 339
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

Query Match 66.9%; Score 117; DB 4; Length 339;
Best Local Similarity 40.3%; Pred. No. 2.6e-08;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGLKWIQE 24
|||
Db 4 KPVSLSYRCPCRFESHVARANKHLKLTNPVCAQIVARLKNNNRQYCIDPKLWQE 63
|||

QY 25 YLEKALN 31
|||
Db 64 YLEKALN 70

RESULT 12

US-09-221-013A-8
Sequence 8, Application US/09221013A
Patent No. 6495740

GENERAL INFORMATION:
APPLICANT: Arioli, Antonio

TITLE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan

FILE REFERENCE: 96-98
CURRENT APPLICATION NUMBER: US/09/221,013A

CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: PCT/AU97/00402

PRIOR FILING DATE: 1997-06-24
PRIOR APPLICATION NUMBER: AU P00699

PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8

LENGTH: 1084
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-221-013A-8

Query Match 34.9%; Score 61; DB 4; Length 1084;
Best Local Similarity 43.5%; Pred. No. 3.6;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFEGGGLKWIQEY 25
: || || : |||
Db 833 IFLSRHCPIMWYGGLKWLRF 855

RESULT 13

US-08-960-048-6
Sequence 6, Application US/08960048C
Patent No. 6271443

GENERAL INFORMATION:
APPLICANT: Stalker, D. et al.

TITLE OF INVENTION: Plant Cellulose Synthase and Promoter

FILE REFERENCE: 15621/01/US
CURRENT APPLICATION NUMBER: US/08/960,048C

CURRENT FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/029,987

PRIOR FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6

LENGTH: 974
TYPE: PRT

ORGANISM: Gossypium hirsutum
US-08-960-048-6

Query Match 34.6%; Score 60.5; DB 3; Length 974;
Best Local Similarity 54.8%; Pred. No. 3.8;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGGLKWIQ 23
: || || : |||
Db 721 IFLSRHCPIMWYGRGGLKWLQ 742

RESULT 14
US-09-838-586-6
Sequence 6, Application US/09838586
Patent No. 6576818

GENERAL INFORMATION:
APPLICANT: Stalker, D. et al.

TITLE OF INVENTION: Plant Cellulose Synthase and Promoter

FILE REFERENCE: 15621/02/US
CURRENT APPLICATION NUMBER: US/09/838,586

CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/029,987

PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 08/960,048

PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6

LENGTH: 974
TYPE: PRT

ORGANISM: Gossypium hirsutum
US-09-838-586-6

Query Match 34.6%; Score 60.5; DB 4; Length 974;
Best Local Similarity 54.5%; Pred. No. 3.8;
Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGGLKWIQ 23
: || || : |||

Db 721 IFLSRHCPWYGGGRLKWLQ 742

RESULT 15
US-09-252

US-09-252-991A-25662
; Sequence 25662, Application US/09252991A

; Sequence 25662, Application US/09252991A
; Patent No. 6551795

; Patent No. 6551795
; GENERAL INFORMATION:

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/ FACILITY NO. 0001700
; GENERAL INFORMATION:
; APPLICANT: Marc J.

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; GENERAL INFORMATION:
; APPLICANT:  Marc J.  Rubenfield et al.
; TITLE OF INVENTION:  NUCLEIC ACID AND

```

APPLICANT: MATC U.
 INVENTOR: KUDENILIDZE ET AL.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196 136

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; TITLE OF INVENTION: AERUGI
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER:

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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1000-03-18

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; CURRENT APPLICATION NUMBER: US/C
; CURRENT FILING DATE: 1999-02-18

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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIORITY APPLICATION NUMBER: US
;; PRIORITY FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-07-27

PRIOR AFFILIATION NUMBER: 0
 PRIOR FILING DATE: 1998-07-
 NUMBER OF SEO ID NOS: 33142

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; PRIOR FILLING D
; NUMBER OF SEQ
; SEQ ID NO 25662

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; NUMBER OF SE
; SEQ ID NO 256
; LENGTH. 535

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; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRP

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; LENGTH: 535
; TYPE: PRT
; ADDRESS: 00000000

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ORGANISM: Pseudo
US-09-252-991A-25662

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Best Local Similarity	43.3%;	Pred. NO. 4.6;		

Query match	33.1%	Score 30, 22
Best Local Similarity	43.3%	Pred. No. 4.6;
Matches 13: Conservative		1; Mismatches

Best Local Similarity	43.36	Filet. NO. 4.0
Matches	13	Conservative
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Db 265 PYPDYRCFGLGGEAGVKANLHYLENLLN 294

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Search completed: October 9, 2003, 09:22:07
Job time : 30 secs
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Job time : 30 secs

Thu Oct 9 16:39:00 2003

us-09-835-107a-11.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 09:18:21 : Search time 375 Seconds
(without alignments)
13.320 Million cell updates/sec

Title: US-09-835-107A-11
Perfect score: 175
Sequence: 1 KPVSLSYRCRPFGGGGLKWIQYLEKALN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	Published Applications AA:*
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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
18:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175	100.0	31	10	US-09-835-107-13
2	175	100.0	31	10	US-09-835-107-15
3	175	100.0	31	10	US-09-835-107-20
4	175	100.0	31	10	US-09-835-107-21
5	175	100.0	31	10	US-09-835-107-22
6	175	100.0	31	10	US-09-835-107-23
7	175	100.0	31	10	US-09-835-107-26
8	175	100.0	31	10	US-09-835-107-27
9	175	100.0	31	12	US-10-086-177A-13
10	175	100.0	31	12	US-10-086-177A-15
11	175	100.0	31	12	US-10-086-177A-20
12	175	100.0	31	12	US-10-086-177A-21
13	175	100.0	31	12	US-10-086-177A-22
14	175	100.0	31	12	US-10-086-177A-23
15	175	100.0	31	12	US-10-086-177A-26

16	175	100.0	31	12	US-10-086-177A-27	Sequence 27, Appl
17	172	98.3	31	10	US-09-835-107-24	Sequence 24, Appl
18	172	98.3	31	10	US-09-835-107-25	Sequence 25, Appl
19	172	98.3	31	12	US-10-086-177A-24	Sequence 24, Appl
20	172	98.3	31	12	US-10-086-177A-25	Sequence 25, Appl
21	166	94.9	31	10	US-09-852-424-74	Sequence 74, Appl
22	166	94.9	31	10	US-09-852-424-122	Sequence 122, App
23	166	94.9	31	10	US-09-852-424-124	Sequence 124, App
24	166	94.9	31	10	US-09-852-424-133	Sequence 133, App
25	166	94.9	31	10	US-09-852-424-134	Sequence 134, App
26	166	94.9	31	10	US-09-852-424-135	Sequence 135, App
27	163.5	93.4	34	10	US-09-835-107-19	Sequence 19, Appl
28	163.5	93.4	34	10	US-09-835-107-17	Sequence 17, Appl
29	163.5	93.4	34	12	US-10-086-177A-17	Sequence 17, Appl
30	163.5	93.4	34	12	US-10-086-177A-19	Sequence 19, Appl
31	162	92.6	31	10	US-09-852-424-95	Sequence 95, Appl
32	161	92.0	31	10	US-09-852-424-79	Sequence 79, Appl
33	161	92.0	31	10	US-09-852-424-94	Sequence 94, Appl
34	160	91.4	31	10	US-09-852-424-97	Sequence 97, Appl
35	159	90.9	31	10	US-09-852-424-78	Sequence 78, Appl
36	159	90.9	31	10	US-09-852-424-81	Sequence 81, Appl
37	158.5	90.6	30	10	US-09-835-107-12	Sequence 12, Appl
38	158.5	90.6	30	10	US-09-835-107-14	Sequence 14, Appl
39	158.5	90.6	30	12	US-10-086-177A-12	Sequence 12, Appl
40	158.5	90.6	30	12	US-10-086-177A-14	Sequence 14, Appl
41	158	90.3	31	10	US-09-852-424-96	Sequence 96, Appl
42	156	89.1	31	10	US-09-852-424-80	Sequence 80, Appl
43	156	89.1	33	10	US-09-835-107-16	Sequence 16, Appl
44	156	89.1	33	10	US-09-835-107-18	Sequence 18, Appl
45	156	89.1	33	12	US-10-086-177A-16	Sequence 16, Appl

RESULT 1

US-09-835-107-13

Sequence 13, Application US/09835107

Patent No. US20020165123A1

GENERAL INFORMATION:

APPLICANT: Tudean, Christopher R.

APPLICANT: Merzoud, Ahmed

APPLICANT: Arab, Lakhdar

APPLICANT: Saxena, Geeta

APPLICANT: Eaves, Connie J.

APPLICANT: Cashman, Johanne

APPLICANT: Clark-Lewis

APPLICANT: Salari, Hassan

TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS

FILE REFERENCE: SMAR012

CURRENT APPLICATION NUMBER: US/09/835,107

CURRENT FILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: CA 2,305,036

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US 60/232,425

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: CA 2,335,109

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 31

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (16)..(19)

OTHER INFORMATION: Spacer monomers (such as the illustrated glycine G's) may be used in variable numbers, such as 2, 3

OTHER INFORMATION: or 4 glycines.

OTHER INFORMATION: Synthesised in Laboratory.

OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013

US-09-835-107-13

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Query Match      100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFEGGGGLKWIQIYELKALN 31
DB 1 KPVSLSYRCPCRFEGGGGLKWIQIYELKALN 31

RESULT 2
US-09-835-107-15
; Sequence 15, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: Synthesised in Laboratory;
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide; or CTCED0017
; NAME/KEY: MOD.RES
; LOCATION: (31)
; OTHER INFORMATION: AMIDATION
; US-09-835-107-15

Query Match      100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFEGGGGLKWIQIYELKALN 31
DB 1 KPVSLSYRCPCRFEGGGGLKWIQIYELKALN 31

RESULT 3
US-09-835-107-20
; Sequence 20, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis

```

```

; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (24)..(28)
; OTHER INFORMATION: cyclized, for example glutamate (E) and lysine (K)
; OTHER INFORMATION: residues may be joined by side chain cyclization
; OTHER INFORMATION: using a lactam formation procedure.
; OTHER INFORMATION: Synthesised in Laboratory;
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF(55-67)-E24/K28-cyclic acid
; US-09-835-107-20

Query Match      100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFEGGGGLKWIQIYELKALN 31
DB 1 KPVSLSYRCPCRFEGGGGLKWIQIYELKALN 31

RESULT 4
US-09-835-107-21
; Sequence 21, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)

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; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (20)..(24)
; OTHER INFORMATION: cyclized, for example glutamate (E) and lysine (K)
; OTHER INFORMATION: residues may be joined by side chain cyclization
; OTHER INFORMATION: using a lactam formation.
; OTHER INFORMATION: synthesized in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic acid
US-09-835-107-21

Query Match          100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPFRFFGGGGLKMIQYLEKALN 31
DB 1 KPVSLSYRCPFRFFGGGGLKMIQYLEKALN 31

RESULT 5
US-09-835-107-22
; Sequence 22, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (24)..(28)
; OTHER INFORMATION: cyclized, for example (E) and lysine (K) residues
; OTHER INFORMATION: may be joined by side chain cyclization using a
; OTHER INFORMATION: lactam formation procedure.
; OTHER INFORMATION: synthesized in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-E24/K28-cyclic
; OTHER INFORMATION: amide: or CTC0022
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: AMIDATION
US-09-835-107-22

Query Match          100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KPVSLSYRCPFRFFGGGGLKMIQYLEKALN 31
DB 1 KPVSLSYRCPFRFFGGGGLKMIQYLEKALN 31

RESULT 6
US-09-835-107-23
; Sequence 23, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (15)..(18)
; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
; OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
; OTHER INFORMATION: or 4 glycines.
; NAME/KEY: DOMAIN
; LOCATION: (20)..(24)
; OTHER INFORMATION: cyclized, for example glutamate (E) and lysine
; OTHER INFORMATION: (K) residues may be joined by side chain
; OTHER INFORMATION: cyclization using a lactam formation procedure.
; OTHER INFORMATION: synthesized in Laboratory:
; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic
; OTHER INFORMATION: amide: or CTC0021
; NAME/KEY: MOD_RES
; LOCATION: (31)
; OTHER INFORMATION: AMIDATION
US-09-835-107-23

Query Match          100.0%; Score 175; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPFRFFGGGGLKMIQYLEKALN 31
DB 1 KPVSLSYRCPFRFFGGGGLKMIQYLEKALN 31

RESULT 7
US-09-835-107-26
; Sequence 26, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
```



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APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SWAR012
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: Spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DISULFID
LOCATION: (9)..(11)
OTHER INFORMATION: cysteine residues may for example be involved in
OTHER INFORMATION: bridge formation
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic acid
US-09-835-107-26

Query Match
Best Local Similarity 100.0%; Score 175; DB 10; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31

RESULT 8
US-09-835-107-27
Sequence 27, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Atab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SWAR012
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
```

```
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DISULFID
LOCATION: (9)..(11)
OTHER INFORMATION: Cysteine residues may for example be involved in
OTHER INFORMATION: bridge formation.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic amide
NAME/KEY: MOD_RES
LOCATION: (31)
OTHER INFORMATION: AMIDATION
US-09-835-107-27

Query Match
Best Local Similarity 100.0%; Score 175; DB 10; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31

RESULT 9
US-10-086-177A-13
Sequence 13, Application US/10086177A
Patent No. US20030148940A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/10/086,177A
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesised in Laboratory: SDF-1 (1-14) - (G)
OTHER INFORMATION: 3-SDF-1 (55-67) acid: or CTCSE0013
US-10-086-177A-13

Query Match
Best Local Similarity 100.0%; Score 175; DB 12; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31
DB 1 KPVSLSYRCPCRFPGGGGLKWIQYLEKALN 31

RESULT 10
US-10-086-177A-15
Sequence 15, Application US/10086177A
Patent No. US20030148940A1
GENERAL INFORMATION:
```

```

; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; US-10-086-177A-15

Query Match
Best Local Similarity 100.0%; Score 175; DB 12; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSTRCPCRFPGGGGLKMIQIYLEKALN 31
DB 1 KPVSLSTRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 11
US-10-086-177A-20
; Sequence 20, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; US-10-086-177A-20
```

```

; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid
; US-10-086-177A-20

Query Match
Best Local Similarity 100.0%; Score 175; DB 12; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSTRCPCRFPGGGGLKMIQIYLEKALN 31
DB 1 KPVSLSTRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 12
US-10-086-177A-21
; Sequence 21, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; US-10-086-177A-21

Query Match
Best Local Similarity 100.0%; Score 175; DB 12; Length 31;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSTRCPCRFPGGGGLKMIQIYLEKALN 31
DB 1 KPVSLSTRCPCRFPGGGGLKMIQIYLEKALN 31

RESULT 13
US-10-086-177A-22
; Sequence 22, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
```

```

; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
US-10-086-177A-22
; FILE REFERENCE: SMAR-012CIP
```

```

Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4,9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31
```

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RESULT 14
US-10-086-177A-23
; Sequence 23, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid: or CTCED0021
US-10-086-177A-23
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```

Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4,9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31
```

```

RESULT 15
US-10-086-177A-26
; Sequence 26, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - C9/C11-cyclic acid
US-10-086-177A-26
```

```

Query Match          100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4,9e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31
Db      1 KPVSLSYRCPCRFEGGGGLKWIQIYLEKALN 31
```

```

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Job time : 375 secs
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